

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 28, 2000, 09:54:51 ; Search time 60.85 Seconds  
(Without alignments)  
204.088 Million cell updates/sec

Title: US-09-157-984-1  
731  
Sequence: 1 KANDFLHRCGYSCDSEEHV.....RFRINACVYLRSNWRH 133

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL\_14:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mhc:\*  
8: sp\_mammal:\*  
9: sp\_organelle:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	731	100.0	140	13	093474 cyprinus ca
2	429	58.7	286	13	091988 xiphophorus
3	368.5	50.4	241	4	09UKR8 homo sapien
4	261.5	35.8	87	6	09TNC3 cervus elap
5	259	35.4	247	6	097759 allurus ful
6	249	34.1	270	13	09YH42 brachydiano
7	244.5	33.4	324	5	09XY95 lampetra fl
8	228	31.2	101	6	09TTR22 macaca fusc
9	160.5	22.0	85	6	002790 macropus fu
10	157.5	21.5	42	13	042312 cyprinus ca
11	154.5	21.1	85	6	002792 notoryctes
12	154.5	21.1	85	6	002798 orithorhyn
13	154.5	21.1	85	6	002798 petaurus br
14	154.5	21.1	85	6	002801 tachyglossu
15	154.5	21.1	85	6	013104 cercartetus
16	154.5	21.1	85	6	013105 dasyuroides
17	154.5	21.1	85	6	013114 isodon mac
18	154.5	21.1	85	6	013122 tarsipes ro
19	153.5	21.0	85	6	002803 trichosurus

20	135.5	18.5	42	6	002802 trichosurus
21	134.5	18.4	42	6	002794 orithorhyn
22	134.5	18.4	42	6	002800 tachyglossu
23	124	17.0	42	13	013118 protoplerus
24	107	14.6	42	13	042314 cyprinus ca
25	106	14.5	43	13	013117 protoplerus
26	97	13.3	43	13	013119 protoplerus
27	86	11.8	43	13	042313 cyprinus ca
28	80	10.9	43	5	09XY96 myxine glut
29	79.5	10.9	2946	5	018857 caenorhabdi
30	77	10.5	129	11	09WU16 mesocricetu
31	77	10.5	1081	3	042696 candida alb
32	77	10.5	1081	3	074271 candida alb
33	77	10.5	1081	3	09URL9 candida alb
34	76.5	10.5	1081	3	093851 candida alb
35	73.5	10.1	422	12	066733 equine infe
36	73.5	10.1	1138	12	09W7U6 equine infe
37	73.5	10.1	1146	12	089468 equine infe
38	73.5	10.1	1146	12	089472 equine infe
39	73.5	10.1	1762	11	088521 rattus norv
40	73	10.0	1298	3	001318 neurospora
41	73	10.0	1298	3	001309 neurospora
42	72	9.8	212	1	028332 archaeoglob
43	71.5	9.8	801	3	09UN8 fusarium so
44	71.5	9.8	1935	13	090339 cyprinus ca
45	71.5	9.8	1938	4	09UKX3 homo sapien

## ALIGNMENTS

RESULT 1  
093474 ID 093474 PRELIMINARY: PRT: 140 AA.  
AC 093474:  
DT 01-NOV-1998 (TRENBLREL. 08, Created)  
DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)  
DT 01-JUN-2000 (TRENBLREL. 14, Last annotation update)  
DE NGF/NT-6-LIKE NEUTROPHILIN (FRAGMENT).  
GN NNT.  
OS Cyprinus carpio (Common carp).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Cyprinidae; Cyprinidae; Cyprinus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lai K.-O., Fu W.-Y., Ip F.C.F., Ip N.Y.;  
RT "Cloning and expression of a novel neutrophilin, NT-7, from carp.";  
RT Mol. Cell. Neurosci. 11:64-76(1998).  
DR EMBL: U94949; AAC25632.1; -.  
DR HSSP: P01139; 1B7C.  
DR INTERPRO: IPR002072; -.  
DR PFM: PFM0243; NGR; 1.  
FT NON\_TER  
SQ SEQUENCE 140 AA; 15855 MW; 3F5E0BCE2601B0FC CRC64;

Query Match 100.0%; Score 731; DB 13; Length 140;  
Best Local Similarity 100.0%; Pred. No. 6.3e-72;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	KANDFLHRCGYSCDSEEHVNLQATDLRGNEVVLPHVRINNVKKQMFETTCRVS	60
DB	8	KANDFLHRCGYSCDSEEHVNLQATDLRGNEVVLPHVRINNVKKQMFETTCRVS	67
QY	61	KPIGAPKPGCGVSGVRACTSCGIDNEHNSCTNVHTVRALTSKNOJAMFIRINA	120
DB	68	KPIGAPKPGCGVSGVRACTSCGIDNEHNSCTNVHTVRALTSKNOJAMFIRINA	127
QY	121	ACVCLVRSNWRH 133	
DB	128	ACVCLVRSNWRH 140	







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Db 1 SISEWVTAADKKTAAVDSGGTIVTLEKVPVPGQLKQFEYERKC--NPMGYTKRG----- 53
QY 74 GYKACTSSCRGIDNEHNSYCTNVHTFYRALT 105
Db 54 -----CRGIDKRRHNSCRRTQSYVRALT 77

RESULT 12
ID 002795 PRELIMINARY; PRT; 85 AA.
AC 002795;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, last annotation update)
DE BRAIN-DERIVED NEUROTROPHIC FACTOR (FRAGMENT).
GN BDNF.
OS Ornithorhynchus anatinus (Duckbill platypus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
[1]
SEQUENCE FROM N.A.
RA Kullander K., Carlson B., Hallbook F.;
RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
EMBL: U93376; AAB58681.1; -.
DR HSSP: P23560; IBBM.
DR INTERPRO: IPR002072; -.
PFAM: PF00243; NGF; 1.
DR PROSITE: PS00248; NGF; 1.
FT NON_TER 1 1
FT NON_TER 85 85
SQ SEQUENCE 85 AA; 9604 MW; 33754EA01520B661 CRC64;

Query Match 21.1%; Score 154.5; DB 6; Length 85;
Best Local Similarity 40.2%; Pred. No. 1.2e-09;
Matches 37; Conservative 6; Mismatches 32; Indels 17; Gaps 3;

QY 16 SEEHVY--GNLQADDLRGNEVTVLPHVAINNVKKOMQYETTCRKRPIGAPKPGQGV 73
Db 1 SISEWVTAADKKTAAVDSGGTIVTLEKVPVPGQLKQFEYERKC--NPMGYTKRG----- 53
QY 74 GYKACTSSCRGIDNEHNSYCTNVHTFYRALT 105
Db 54 -----CRGIDKRRHNSCRRTQSYVRALT 77

RESULT 13
ID 002798 PRELIMINARY; PRT; 85 AA.
AC 002798;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, last annotation update)
DE BRAIN-DERIVED NEUROTROPHIC FACTOR (FRAGMENT).
GN BDNF.
OS Petarus breviceps (Australian sugar glider).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Petauridae; Petarus.
[1]
SEQUENCE FROM N.A.
RA Kullander K., Carlson B., Hallbook F.;
RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
EMBL: U93377; AAB58682.1; -.
DR HSSP: P23560; IBBM.
DR INTERPRO: IPR002072; -.
PFAM: PF00243; NGF; 1.
DR PROSITE: PS00248; NGF; 1.
FT NON_TER 1 1
FT NON_TER 85 85
SQ SEQUENCE 85 AA; 9604 MW; 33754EA01520B661 CRC64;

Query Match 21.1%; Score 154.5; DB 6; Length 85;
Best Local Similarity 40.2%; Pred. No. 1.2e-09;
Matches 37; Conservative 6; Mismatches 32; Indels 17; Gaps 3;

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Query Match      21.1%; Score 154.5; DB 6; Length 85;
Best Local Similarity 40.2%; Pred. No. 1.2e-09;
Matches 37; Conservative 6; Mismatches 32; Indels 17; Gaps 3;

OY 16 SEEHV--GNLTQATDLRGNEVTYLPKRNINNVKKOMFEYTTTCRVSPICAPKPGGVS 73
    |  | :  | -  | -  | | | | :  | | | | |  | | | | |  |
Db 1 SISEWTAALFKRTAVDMSSGTIVLEKVPKPKGLKOYEETKC--NPMGYTEG----- 53

OY 74 GVKAGTSCFCIDNEHWNYSCTNVHTFVRALT 105
    ||||| |||| |  :::||||
Db 54 -----CGCIDKRHMNSOCRTTOSYVRALT 77

RESULT 14
002801 PRELIMINARY; PRT; 85 AA.
AC 002801;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE BRAIN-DERIVED NEUROTROPHIC FACTOR (FRAGMENT).
GN BDNF.
OS Tachyloesus aculeatus aculeatus (Australian echidna).
OC Chordata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Monotremata; Tachylossidae; Tachyloesus.
RN [1]
RP SEQUENCE FROM N.A.
RA Kullander K., Carlson B., Hallbook F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93383; AAB58688.1; -.
DR HSSP; P23560; 1B8M.
DR INTERPRO; IPR0C2072; -.
PFAM; PF00243; NGF; 1.
DR PROSITE; PS00248; NGF; 1.
FT NON_TER 1
FT NON_TER 85
SQ SEQUENCE 85 AA; 9604 MW; 33754EA01520B661 CRC64;

Query Match      21.1%; Score 154.5; DB 6; Length 85;
Best Local Similarity 40.2%; Pred. No. 1.2e-09;
Matches 37; Conservative 6; Mismatches 32; Indels 17; Gaps 3;

OY 16 SEEHV--GNLTQATDLRGNEVTYLPKRNINNVKKOMFEYTTTCRVSPICAPKPGGVS 73
    |  | :  | -  | -  | | | | :  | | | | |  | | | | |  |
Db 1 SISEWTAADKRTAVDMSSGTIVLEKVPKPKGLKOYEETKC--NPMGYTKES---- 53

OY 74 GVKAGTSCFCIDNEHWNYSCTNVHTFVRALT 105
    ||||| |||| |  :::||||
Db 54 -----CRGIDKRHMNSOCRTTOSYVRALT 77

RESULT 15
013104 PRELIMINARY; PRT; 85 AA.
AC 013104;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE BRAIN-DERIVED NEUROTROPHIC FACTOR (FRAGMENT).
GN BDNF.
OS Cercartetus laiidus.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Burramyidae; Cercartetus.
RN [1]
RP SEQUENCE FROM N.A.
RA Kullander K., Carlson B., Hallbook F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93378; AAB58683.1; -.
DR HSSP; P23560; 1B8M.
DR INTERPRO; IPR0C2072; -.
PFAM; PF00243; NGF; 1.
DR PROSITE; PS00248; NGF; 1.
FT NON_TER 1

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FT	NON_TER	85	85
SQ	SEQUENCE	85 AA;	9604 MW; 33754EA01520B661 CRC64;

Query Match	21.1%	Score 154.5	DB 6	Length 85
Best Local Similarity	40.2%	Pred. No. 1.2e-09		
Matches 37, Conservative	6	Mismatches 32	Indels 17	Gaps 3

[illegible]

Search completed: October 28, 2000, 12:38:30  
Job time: 9819 sec